



(A)

/home/ru.../carpenda/templ/ss.DNA40370 (1650 bp)

Sequences producing High-scoring Segment Pairs:	Frame	Score	Match	Pct	E-val
1 P_AAF72416 Human PRO302 cDNA.	+	1650	1650	100	0.0
2 P_AAF30502 Human PRO302 cDNA clone DNA40370-1217.	+	1650	1650	100	0.0
3 P_AAA13199 PRO302, vitellogenin carboxypeptidase ho	+	1650	1650	100	0.0
4 P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217.	+	1650	1650	100	0.0
5 P_AAX25445 Human PRO216 cDNA clone UNQ265.	+	1650	1650	100	0.0
6 AX098272 Sequence 11 from Patent WO0119987.	+	1650	1650	100	0.0
7 NM_021626 Homo sapiens serine carboxypeptidase 1 p	+	1640	1646	100	0.0
8 AF282618 Homo sapiens serine carboxypeptidase 1 p	+	1640	1646	100	0.0
9 AK027373 Homo sapiens cDNA FLJ14467 fis, clone MA	+	1637	1640	100	0.0
10 AF113214 Homo sapiens MSTP034 mRNA, complete cds.	+	1594	1594	100	0.0
11 P_AAC75884 Human ORFX ORF1439 polynucleotide sequen	+	1543	1619	99	0.0

>1 P_AAF72416 Human PRO302 cDNA. (1650 bp) [1 seg]
Score = 1650 (3271 bits), Expect = 0.0
Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

DNA40370	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
P_AAF72416	1	GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCC
DNA40370	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCGTAACGCAGGAGCTGTCATT
P_AAF72416	61	GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCGTAACGCAGGAGCTGTCATT
DNA40370	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
P_AAF72416	121	GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC
P_AAF72416	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC
DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
P_AAF72416	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
DNA40370	301	GAAATTTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAAACACCTGGCTCCAGGCTGCC
P_AAF72416	301	GAAATTTGGGCCCCCTTGACAGTGATCTCAAACCACGAAAAACACCTGGCTCCAGGCTGCC
DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
P_AAF72416	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAF72416	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
DNA40370	481	TTCAAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
P_AAF72416	481	TTCAAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGA
DNA40370	541	GGAAAAATGGCAGCTGGCATTTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
P_AAF72416	541	GGAAAAATGGCAGCTGGCATTTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC
DNA40370	601	AAGTGCACACTTTTGGCGGGGTTGCCCTTGGGTGATTCCTGGATCTCCCTGTGATTGCGGT
P_AAF72416	601	AAGTGCACACTTTTGGCGGGGTTGCCCTTGGGTGATTCCTGGATCTCCCTGTGATTGCGGT

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DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAF72416	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAF72416	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
P_AAF72416	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAF72416	841	TATAACATCTTAACTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAF72416	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATC
P_AAF72416	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGT
P_AAF72416	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGT
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
P_AAF72416	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA
P_AAF72416	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
P_AAF72416	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
P_AAF72416	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
DNA40370	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
P_AAF72416	1321	GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
P_AAF72416	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
DNA40370	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTTCCCCTGTATCTAACTGGGGCTGT
P_AAF72416	1441	GAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTTCCCCTGTATCTAACTGGGGCTGT
DNA40370	1501	GATCAAGAAGGTTCTTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
P_AAF72416	1501	GATCAAGAAGGTTCTTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1561	TGGAAATTATTTCTGCTTTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
P_AAF72416	1561	TGGAAATTATTTCTGCTTTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

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BLAST RESULTS A-2

DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA

P_AAF72416 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>2 P_AAF30502 Human PRO302 cDNA clone DNA40370-1217. DNA, PAT 29-MAY-2001 (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

P_AAF30502 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCTGAACGCAGGAGCTGTCATT

P_AAF30502 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCTGAACGCAGGAGCTGTCATT

DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

P_AAF30502 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

P_AAF30502 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC

DNA40370 241 CTGGTCATGTGGCTTCAGGCGGTCCAGGCGGTCTAGCACTGGATTGGAACCTTTGAG

P_AAF30502 241 CTGGTCATGTGGCTTCAGGCGGTCCAGGCGGTCTAGCACTGGATTGGAACCTTTGAG

DNA40370 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC

P_AAF30502 301 GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC

DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT

P_AAF30502 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGT

DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTC

P_AAF30502 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTGAAGACCTTC

DNA40370 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTTCTACATTTTCTCAGAGTCTATGGA

P_AAF30502 481 TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTTCTACATTTTCTCAGAGTCTATGGA

DNA40370 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC

P_AAF30502 541 GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATC

DNA40370 601 AAGTGCACCTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCTGTTGATTGCGTG

P_AAF30502 601 AAGTGCACCTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCTGTTGATTGCGTG

DNA40370 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCTCGAAGACAAAGGTCTGGCAGAG

P_AAF30502 661 CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTCTCTCGAAGACAAAGGTCTGGCAGAG

DNA40370 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCGGTAAATAAGGGGCTCTACAGAGAGGCC

P_AAF30502 721 GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCGGTAAATAAGGGGCTCTACAGAGAGGCC

DNA40370 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGGGTTGAATTC

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BLAST RESULTS A-3

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BLAST RESULTS A-4

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P_AAF30502 781 ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
 DNA40370 841 TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA

 P_AAF30502 841 TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
 DNA40370 901 CAGAGCCACCTAGTTTGTCTTTGTCTGAGCGCCACGTGAGACACCTACAACGAGATGCCTTA

 P_AAF30502 901 CAGAGCCACCTAGTTTGTCTTTGTCTGAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
 DNA40370 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC

 P_AAF30502 961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
 DNA40370 1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC

 P_AAF30502 1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
 DNA40370 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGATAATGGACA

 P_AAF30502 1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGATAATGGACA
 DNA40370 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAACTGAAGTGGCC

 P_AAF30502 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAACTGAAGTGGCC
 DNA40370 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCTTAAATCTTT

 P_AAF30502 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCTTAAATCTTT
 DNA40370 1261 GAAACATCTGCTTTTGTCAAGTCTTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT

 P_AAF30502 1261 GAAACATCTGCTTTTGTCAAGTCTTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCT
 DNA40370 1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

 P_AAF30502 1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
 DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

 P_AAF30502 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
 DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

 P_AAF30502 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
 DNA40370 1501 GATCAAGAAGGTTC TGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

 P_AAF30502 1501 GATCAAGAAGGTTC TGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
 DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTG

 P_AAF30502 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTG
 DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA

 P_AAF30502 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>3 P_AAA13199 PRO302, vitellogenic carboxypeptidase homologue nucleotide sequence, (1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1 1650,1650, Strand ++

DNA40370 1 GCTTGTGTGCTGATGCTGGCCCTGGCGTACTTGTTCATGGAGCTGGGCACTGGGGGCTCTCCG

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*****
P_AAA13199      1  GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCCGGCGCTCTCCC
DNA40370      61  GTCCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCCTGAACGCAGGAGCTGTCATT
*****
P_AAA13199      61  GTCCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCCTGAACGCAGGAGCTGTCATT
DNA40370     121  GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
P_AAA13199     121  GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
DNA40370     181  TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
*****
P_AAA13199     181  TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
DNA40370     241  CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
*****
P_AAA13199     241  CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAG
DNA40370     301  GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCC
*****
P_AAA13199     301  GAAATTGGGCCCCTTGACAGTGATCTCAAACCACGAAAACACCTGGCTCCAGGCTGCC
DNA40370     361  AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTG
*****
P_AAA13199     361  AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTG
DNA40370     421  GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAACCTT
*****
P_AAA13199     421  GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAACCTT
DNA40370     481  TTCAGTTGCCACAAGAATTCAGACAGTTCATTCTACATTTCTCAGAGTCCCTATGGA
*****
P_AAA13199     481  TTCAGTTGCCACAAGAATTCAGACAGTTCATTCTACATTTCTCAGAGTCCCTATGGA
DNA40370     541  GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
*****
P_AAA13199     541  GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATC
DNA40370     601  AAGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTCCTGGATCTCCCTGTGATTCGGTG
*****
P_AAA13199     601  AAGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTCCTGGATCTCCCTGTGATTCGGTG
DNA40370     661  CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
*****
P_AAA13199     661  CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370     721  GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
*****
P_AAA13199     721  GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370     781  ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
*****
P_AAA13199     781  ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
DNA40370     841  TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
*****
P_AAA13199     841  TATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370     901  CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
*****
P_AAA13199     901  CAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370     961  AGCCAGCTGATGAATGGGTCCTATCAGAAAGAGCTCAAAATTTATTCCTGAGGATCAATCC

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BLAST RESULTS A-5

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A-6
SINSE 15774

TECH CENTER 1600/2900

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*****
P_AAA13199   961 AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAAT'TAT'TCCTGAGGATCAATCC
DNA40370     1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
*****
P_AAA13199   1021 TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370     1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
*****
P_AAA13199   1081 ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA40370     1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCCTGGGTGCCGAAACTGAAGTGGCCA
*****
P_AAA13199   1141 CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCCTGGGTGCCGAAACTGAAGTGGCCA
DNA40370     1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
*****
P_AAA13199   1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
DNA40370     1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
*****
P_AAA13199   1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
DNA40370     1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
*****
P_AAA13199   1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
DNA40370     1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTTGGGGCACAGAGCT
*****
P_AAA13199   1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCCTTGGGGCACAGAGCT
DNA40370     1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
*****
P_AAA13199   1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
DNA40370     1501 GATCAAGAAGGTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
P_AAA13199   1501 GATCAAGAAGGTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370     1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
*****
P_AAA13199   1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
DNA40370     1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
P_AAA13199   1621 ATCAAAATAAAGGATGATAATAGATATTAA

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>4 P_AAX52258 Protein PRO302 cDNA clone DNA40370-1217. DNA, PAT 25-JUN-1999
(1650 bp) [1 seg]

Score = 1650 (3271 bits), Expect = 0.0

Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/+

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DNA40370      1 GCCTGTTGCTGATGCTGCCGTGCCGTACTTGTTCATGGAGCTGGCACTGCCGGCGCTCTCCC
*****
P_AAX52258     1 GCCTGTTGCTGATGCTGCCGTGCCGTACTTGTTCATGGAGCTGGCACTGCCGGCGCTCTCCC
DNA40370      61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGCCCTGAACGCAGGAGCTGTCAAT
*****
P_AAX52258     61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGCCCTGAACGCAGGAGCTGTCAAT
DNA40370     121 GACTGGCCACACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
*****
P_AAX52258    121 GACTGGCCACACAGAGGAGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

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DNA40370	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
P_AAX52258	181	TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCC
DNA40370	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
P_AAX52258	241	CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
DNA40370	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
P_AAX52258	301	GAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCC
DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
P_AAX52258	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGT
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX52258	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
DNA40370	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATGGA
P_AAX52258	481	TTCAGTTGCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCATGGA
DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
P_AAX52258	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATC
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG
P_AAX52258	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTGGATCTCCCCTGTTGATTCCGGTG
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX52258	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX52258	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
P_AAX52258	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC
DNA40370	841	TATAACATCTTAAGTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX52258	841	TATAACATCTTAAGTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX52258	901	CAGAGCCACCTAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTTGAGGATCAATCC
P_AAX52258	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCTTGAGGATCAATCC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
P_AAX52258	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370	1081	ATTAGCATTTGTGGACGAGTTGCTGGAGGCGATCAACCTGACGGTGTATAATGGACAG
P_AAX52258	1081	ATTAGCATTTGTGGACGAGTTGCTGGAGGCGATCAACCTGACGGTGTATAATGGACAG

BLAST RESULTS A-F

DNA40370 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA
 P_AAX52258 1141 CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCCTGGGTGCGGAAACTGAAGTGGCCA

DNA40370 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG
 P_AAX52258 1201 GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG

DNA40370 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
 P_AAX52258 1261 GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

DNA40370 1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
 P_AAX52258 1321 GGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
 P_AAX52258 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
 P_AAX52258 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

DNA40370 1501 GATCAAGAAGGTTCCTGACCAGCTTCTGCAGAGGATAAAATCATTTGTCTCTGGAGGCAATT
 P_AAX52258 1501 GATCAAGAAGGTTCCTGACCAGCTTCTGCAGAGGATAAAATCATTTGTCTCTGGAGGCAATT

DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG
 P_AAX52258 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG

DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA
 P_AAX52258 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>5 P_AAX25445 Human PRO216 cDNA clone UNQ265. (1650 bp) [1 seg]
 Score = 1650 (3271 bits), Expect = 0.0
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC
 P_AAX25445 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCC

DNA40370 61 GTCCCGCGGTGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT
 P_AAX25445 61 GTCCCGCGGTGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATT

DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC
 P_AAX25445 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCC

DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC
 P_AAX25445 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCC

DNA40370 241 CTGGTCATGTGGCTTCAGGCGCGTCCAGGCGGTCTAGCACTGGATTGGAACCTTTGAG
 P_AAX25445 241 CTGGTCATGTGGCTTCAGGCGCGTCCAGGCGGTCTAGCACTGGATTGGAACCTTTGAG

DNA40370 301 GAAATTTGGGCCCTTTGACAGTGATCTCAAAACACGGAAAACCACTGGCTCCAGGCTGCC
 P_AAX25445 301 GAAATTTGGGCCCTTTGACAGTGATCTCAAAACACGGAAAACCACTGGCTCCAGGCTGCC

BLAST RESULTS A-8

DNA40370	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
P_AAX25445	361	AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGT
DNA40370	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
P_AAX25445	421	GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
DNA40370	481	TTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCCTATGGA
P_AAX25445	481	TTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCCTATGGA
DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
P_AAX25445	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCCTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
P_AAX25445	601	AAGTGCAACTTTGCGGGGGTTGCCCTGGGTGATTCTGGATCTCCCCTGTTGATTTCGGTG
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
P_AAX25445	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
P_AAX25445	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
P_AAX25445	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAAC TTC
DNA40370	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
P_AAX25445	841	TATAACATCTTAACTAAAAGCACTCCACGTCTACAATGGAGTCGAGTCTAGAATTCACA
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
P_AAX25445	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
P_AAX25445	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
P_AAX25445	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC
DNA40370	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
P_AAX25445	1081	ATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
P_AAX25445	1141	CTGGATCTCATCGTAGATACCATGGGTGAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA
DNA40370	1201	GAAGTGCCTAAATTCAGTCAGCTGAAAGTGGAAAGGCCCTGTACAGTGACCCCTAAATCTTTG
P_AAX25445	1201	GAAGTGCCTAAATTCAGTCAGCTGAAAGTGGAAAGGCCCTGTACAGTGACCCCTAAATCTTTG
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT
P_AAX25445	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT

BLAST RESULTS A9

DNA40370 1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT

 P_AAX25445 1321 GGTTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT
 DNA40370 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT

 P_AAX25445 1381 CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT
 DNA40370 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT

 P_AAX25445 1441 GAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT
 DNA40370 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT

 P_AAX25445 1501 GATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
 DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG

 P_AAX25445 1561 TGGAAATTATTTCTGCTTCTTAAAAAAACCTAAGATTTTTTAAAAAATTGATTTGTTTTG
 DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA

 P_AAX25445 1621 ATCAAAATAAAGGATGATAATAGATATTAA

>6 AX098272 Sequence 11 from Patent W00119987. (1650 bp) [1 seg]
 Score = 1650 (3271 bits), Expect = 0.0
 Identities = 1650/1650 (100%), at 1,1-1650,1650, Strand +/-

DNA40370 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCC

 AX098272 1 GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCCTCTCCC
 DNA40370 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGCCCTGAACGCAGGAGCTGTCATT

 AX098272 61 GTCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGCCCTGAACGCAGGAGCTGTCATT
 DNA40370 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTTATGTGACGGTCCGCAAGGATGCC

 AX098272 121 GACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTTATGTGACGGTCCGCAAGGATGCC
 DNA40370 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAAGTTCTCAGAAGTGGCC

 AX098272 181 TACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAAGTTCTCAGAAGTGGCC
 DNA40370 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG

 AX098272 241 CTGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAG
 DNA40370 301 GAAATTGGGCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC

 AX098272 301 GAAATTGGGCCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCC
 DNA40370 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAAGTATGTGAATGGTAGTGGT

 AX098272 361 AGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCAAGTATGTGAATGGTAGTGGT
 DNA40370 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC

 AX098272 421 GCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTC
 DNA40370 481 TTCAGTTGGCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGATTCCTATGGA

 AX098272 481 TTCAGTTGGCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGATTCCTATGGA

BLAST RESULTS A-10

DNA40370	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC *****
AX098272	541	GGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATC *****
DNA40370	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTTCGGTG *****
AX098272	601	AAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCGATCTCCCCTGTTGATTTCGGTG *****
DNA40370	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
AX098272	661	CTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAG *****
DNA40370	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
AX098272	721	GTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCC *****
DNA40370	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC *****
AX098272	781	ACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTC *****
DNA40370	841	TATAACATCTTAACATAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA *****
AX098272	841	TATAACATCTTAACATAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAATTCACA *****
DNA40370	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
AX098272	901	CAGAGCCACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTA *****
DNA40370	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC *****
AX098272	961	AGCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCC *****
DNA40370	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
AX098272	1021	TGGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTC *****
DNA40370	1081	ATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
AX098272	1081	ATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAG *****
DNA40370	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA *****
AX098272	1141	CTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCA *****
DNA40370	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
AX098272	1201	GAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTG *****
DNA40370	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
AX098272	1261	GAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCT *****
DNA40370	1321	GGTCATATGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
AX098272	1321	GGTCATATGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACT *****
DNA40370	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
AX098272	1381	CAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCT *****
DNA40370	1441	GAGCTGAGGCGGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****
AX098272	1441	GAGCTGAGGCGGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGT *****

BLAST RESULTS A-11

BLAST RESULTS A-12

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DNA40370 1501 GATCAAGAAGGTCTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
AX098272 1501 GATCAAGAAGGTCTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
*****
DNA40370 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG
*****
AX098272 1561 TGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTTG
*****
DNA40370 1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
AX098272 1621 ATCAAAATAAAGGATGATAATAGATATTAA
*****
>7 NM_021626 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)
(1921 bp) [1 seg]
Score = 1640 (3251 bits), Expect = 0.0
Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/-

DNA40370 2 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
*****
NM_021626 1 CCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCG
*****
DNA40370 62 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
*****
NM_021626 61 TCCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTG
*****
DNA40370 122 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
*****
NM_021626 121 ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
*****
DNA40370 182 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
*****
NM_021626 181 ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCC
*****
DNA40370 242 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
*****
NM_021626 241 TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTTGAGG
*****
DNA40370 302 AAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCCA
*****
NM_021626 301 AAATTGGGCCCCCTTGACAGTGATCTCAAACACGGAAAACACCTGGCTCCAGGCTGCCA
*****
DNA40370 362 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTG
*****
NM_021626 361 GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTCACTTATGTGAATGGTAGTGGTG
*****
DNA40370 422 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
*****
NM_021626 421 CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
*****
DNA40370 482 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAG
*****
NM_021626 481 TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAG
*****
DNA40370 542 GAAAAATGSCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATCA
*****
NM_021626 541 GAAAAATGSCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACGCGAGGGACCATCA
*****
DNA40370 602 AGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTTCCTGGATCTCCCCCTGTTGATTCCGTTGC
*****
NM_021626 601 AGTGCAACTTTGCGGGGGTTGCCCTTGGGTGATTTCCTGGATCTCCCCCTGTTGATTCCGTTGC
*****
DNA40370 662 TCTCCTGGGAGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTTCTGGCAGAGG
*****
NM_021626 661 TCTCCTGGGAGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTTCTGGCAGAGG
*****
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DNA40370	722	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGGCTCTACAGAGAGGCCA
NM_021626	721	TGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGGCTCTACAGAGAGGCCA
DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
NM_021626	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCT
DNA40370	842	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
NM_021626	841	ATAACATCTTAACTAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACAC
DNA40370	902	AGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
NM_021626	901	AGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATGCCTTAA
DNA40370	962	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
NM_021626	961	GCCAGCTCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCT
DNA40370	1022	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
NM_021626	1021	GGGGAGGCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCA
DNA40370	1082	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
NM_021626	1081	TTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGC
DNA40370	1142	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
NM_021626	1141	TGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAG
DNA40370	1202	AACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
NM_021626	1201	AACTGCCTAAATTTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCTAAATCTTTGG
DNA40370	1262	AAACATCTGCTTTTGTCAAGTCCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCTG
NM_021626	1261	AAACATCTGCTTTTGTCAAGTCCCTACAAGAACCCTTGCTTTCTACTGGATTCTGAAAGCTG
DNA40370	1322	GTCATATGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
NM_021626	1321	GTCATATGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTC
DNA40370	1382	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
NM_021626	1381	AGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTG
DNA40370	1442	AGCTGAGGECGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
NM_021626	1441	AGCTGAGGECGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTG
DNA40370	1502	ATCAAGAAAGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
NM_021626	1501	ATCAAGAAAGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATT
DNA40370	1562	GGAAATTAATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGATTTGTTTTGA
NM_021626	1561	GGAAATTAATTTCTGCTTCTTAAAAAACCTAAGATTTTAAAAAATTGATTTGTTTTGA
DNA40370	1622	TCAAAAATAAAGGATGATAATAGATATTA
NM_021626	1621	TCAAAAATAAAGGATGATAATAGATATTA

BLAST RESULTS A-13

>8 AF282618 Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1)
 (1921 bp) [1 seq]
 Score = 1640 (3251 bits), Expect = 0.0
 Identities = 1646/1648 (99%), at 2,1-1649,1648, Strand +/+

DNA40370	2	CCTGTTGCTGATGCTGCCGTGCGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCG
AF282618	1	CCTGTTGCTGATGCTGCCGTGCGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCG
DNA40370	62	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGCGCCTGAACGCAGGAGCTGTCATTG
AF282618	61	TCCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGCGCCTGAACGCAGGAGCTGTCATTG
DNA40370	122	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
AF282618	121	ACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCT
DNA40370	182	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTCCCC
AF282618	181	ACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAGTCCCC
DNA40370	242	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGG
AF282618	241	TGGTCATGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAACCTTGAGG
DNA40370	302	AAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCCA
AF282618	301	AAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACACCTGGCTCCAGGCTGCCA
DNA40370	362	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTG
AF282618	361	GTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTCAAGTTATGTGAATGGTAGTGGTG
DNA40370	422	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
AF282618	421	CCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCT
DNA40370	482	TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCACATTTTCTCAGAGTCCATATGGAG
AF282618	481	TCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCACATTTTCTCAGAGTCCATATGGAG
DNA40370	542	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
AF282618	541	GAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTACAGCGAGGGACCATCA
DNA40370	602	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCTGGATCTCCCCCTGTTGATTCCGTGC
AF282618	601	AGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCTCTGGATCTCCCCCTGTTGATTCCGTGC
DNA40370	662	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
AF282618	661	TCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGG
DNA40370	722	TGTC TAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
AF282618	721	TGTC TAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCA
DNA40370	782	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGGGGTGAACCTCT
AF282618	781	CAGAGCTGTGGGGGAAAGCAGAAATGATCATTTGAACAGAACACAGATGGGGTGAACCTCT
DNA40370	842	ATAACATCTTAAC TAAAAGCACTCCGACCTTACAATGGAGTCGAGTCTAGAATTCACAC

BLAST RESULTS A-A


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*****
AK027373      61 GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
DNA40370     128 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
*****
AK027373     121 CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
DNA40370     188 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
*****
AK027373     181 TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCA
DNA40370     248 TGTGGCTTCAGGGCGGTCCAGGCGGTTCAGCACTGGATTTGGAACTTTGAGGAAATTG
*****
AK027373     241 TGTGGCTTCAGGGCGGTCCAGGCGGTTCAGCACTGGATTTGGAACTTTGAGGAAATTG
DNA40370     308 GGCCCCCTTGACAGTGATCTCAAACACGAAAACCACCTGGCTCCAGGCTGCCAGTCTCC
*****
AK027373     301 GGCCCCCTTGACAGTGATCTCAAACACGAAAACCACCTGGCTCCAGGCTGCCAGTCTCC
DNA40370     368 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATG
*****
AK027373     361 TATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTAGTGGTGCCTATG
DNA40370     428 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
*****
AK027373     421 CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTT
DNA40370     488 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
*****
AK027373     481 GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
DNA40370     548 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCA
*****
AK027373     541 TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCA
DNA40370     608 ACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCT
*****
AK027373     601 ACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATTCGGTGCTCTCCT
DNA40370     668 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
*****
AK027373     661 GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
DNA40370     728 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
*****
AK027373     721 AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
DNA40370     788 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
*****
AK027373     781 TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
DNA40370     843 TCCTAACTAAAAGCACTCCCAAGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
*****
AK027373     841 TCCTAACTAAAAGCACTCCCAAGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
DNA40370     903 ACCTAAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
*****
AK027373     901 ACCTAAGTTTGTCTTTGTGACGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC
DNA40370     968 TCATGAATGGGCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
*****
AK027373     961 TCATGAATGGGCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
DNA40370    1028 GCGTGGCTACCAACGTCTTTGTGAACATTCAGGAGGACTTCATGAACCAACTCATTAGCA

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BLAST RESULTS A-16


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*****
AK027373 1021 GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
DNA40370 1088 TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
*****
AK027373 1081 TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC
DNA40370 1148 TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGCTGC
*****
AK027373 1141 TCATCGTAGATACCATGGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGGCCAGAAGCTGC
DNA40370 1208 CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAAACAT
*****
AK027373 1201 CTAAATTCAGTCAGCTGAAGTGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAAACAT
DNA40370 1268 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
*****
AK027373 1261 CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
DNA40370 1328 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
*****
AK027373 1321 TGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
DNA40370 1388 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
*****
AK027373 1381 AATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACAGAGCTGAGCTGA
DNA40370 1448 GGCCGCTGAAGCTGTAGGAAGCGCCATTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
*****
AK027373 1441 GGCCGCTGAAGCTGTAGGAAGCGCCACTCTCCCTGTATCTAACTGGGGCTGTGATCAAG
DNA40370 1508 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT
*****
AK027373 1501 AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAT
DNA40370 1568 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTGATCAAAA
*****
AK027373 1561 TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGTGTTTGATCAAAA
DNA40370 1628 TAAAGGATGATAATAGATATT
*****
AK027373 1621 TAAAGGATGATAATAGATATT

```

>10 AF113214 Homo sapiens MSTP034 mRNA, complete cds. mRNA, PRI 12-DEC-2000 (1902 bp) [1 seg]

Score = 1594 (3160 bits), Expect = 0.0

Identities = 1594/1594 (100%), at 56,1-1649,1594, Strand +/+

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DNA40370 56 CTCCCGTECCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCGCTGAACGCAGGAGCTG
*****
AF113214 1 CTCCCGTECCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCGCTGAACGCAGGAGCTG
DNA40370 116 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG
*****
AF113214 61 TCATTGACTGGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGG
DNA40370 176 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC
*****
AF113214 121 ATGCCTACATGTTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAAC
DNA40370 236 TGCCCGTGGTCATGTGGCTTCAGGGCGGTTCAGGCGGTTCCTAGCACTGATTTGGAAACT
*****
AF113214 181 TGCCCGTGGTCATGTGGCTTCAGGGCGGTTCAGGCGGTTCCTAGCACTGATTTGGAAACT

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DNA40370	296	TTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGG
AF113214	241	TTGAGGAAATTGGGCCCCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGG
DNA40370	356	CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTTCAGTTATGTGAATGGTA
AF113214	301	CTGCCAGTCTCCTATTTGTGGATAATCCCGTGGGCACTGGGTTTTCAGTTATGTGAATGGTA
DNA40370	416	GTGGTGCCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA
AF113214	361	GTGGTGCCCTATGCCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGA
DNA40370	476	CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT
AF113214	421	CCTTCTTCAGTTGCCACAAAGAATTCCAGACAGTTCCATTCTACATTTTCTCAGAGTCCT
DNA40370	536	ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGA
AF113214	481	ATGGAGGAAAAATGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGA
DNA40370	596	CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATT
AF113214	541	CCATCAAGTGCAACTTTGCGGGGGTTGCCTTGGGTGATTCCCTGGATCTCCCCTGTTGATT
DNA40370	656	CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG
AF113214	601	CGGTGCTCTCCTGGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGG
DNA40370	716	CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG
AF113214	661	CAGAGGTGTCTAAGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAG
DNA40370	776	AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA
AF113214	721	AGGCCACAGAGCTGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGA
DNA40370	836	ACTTCTATAACATCTTAAGTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAAT
AF113214	781	ACTTCTATAACATCTTAAGTAAAAGCACTCCACGCTCTACAATGGAGTCGAGTCTAGAAT
DNA40370	896	TCACACAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATG
AF113214	841	TCACACAGAGCCACCTAGTTTGTCTTTGTGTCAGCGCCACGTGAGACACCTACAACGAGATG
DNA40370	956	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAAGAAGCTCAAAATTATTCCTGAGGATC
AF113214	901	CCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAAGAAGCTCAAAATTATTCCTGAGGATC
DNA40370	1016	AATCCTGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
AF113214	961	AATCCTGGGGAGGCCAGGCTACCAACGCTCTTTGTGAACATGGAGGAGGACTTCATGAAGC
DNA40370	1076	CAGTCATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
AF113214	1021	CAGTCATTAGCATTTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATG
DNA40370	1136	GACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCGCTGGGTGCGGAAACTGAAGT
AF113214	1081	GACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGCGCTGGGTGCGGAAACTGAAGT
DNA40370	1196	GGCCAGAACTGCCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCCTAAAT
AF113214	1141	GGCCAGAACTGCCCTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCCTAAAT

BLAST RESULTS A-19

DNA40370	1256	CTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGA
AF113214	1201	CTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGA
DNA40370	1316	AAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
AF113214	1261	AAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGG
DNA40370	1376	TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
AF113214	1321	TGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCTTGGGGCACA
DNA40370	1436	GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
AF113214	1381	GAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGG
DNA40370	1496	GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
AF113214	1441	GCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGG
DNA40370	1556	CAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTG
AF113214	1501	CAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTTG
DNA40370	1616	TTTTGATCAAAAATAAAGGATGATAATAGATATTA
AF113214	1561	TTTTGATCAAAAATAAAGGATGATAATAGATATTA

>11 P_AAC75884 Human ORFX ORF1439 polynucleotide sequence SEQ ID NO:2877. (1921 bp) [1 seg]

Score = 1543 (3059 bits), Expect = 0.0

Identities = 1619/1642 (98%), Gaps = 3/1642 (0%), at 8,2-1649,1640, Strand +/-

DNA40370	8	GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
P_AAC75884	2	GCTGATGCTGCCGTGCGGTACTTGTTCATGGAGCTGGCACTGCGGCGCTCTCCCGTCCCGC
DNA40370	68	GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
P_AAC75884	62	GGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACTGGC
DNA40370	128	CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
P_AAC75884	122	CCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATGT
DNA40370	188	TCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCACAGAACTGCCCTGGTCA
P_AAC75884	182	TCTGGTGGCTCTATTATGCCACC-ACTCCTGCAAGAACT--TCAGAACTGCCCTGGTCA
DNA40370	248	TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAACTTTGAGGAAATTG
P_AAC75884	239	TGTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAACTTTGAGGAAATTG
DNA40370	308	GGCCCTTGACAGTGATCTCAAACACGGAAACCACTGGCTCCAGGCTGCCAGTCTCC
P_AAC75884	299	GGCCCTTGACAGTGATCTCAAACACGGAAACCACTGGCTCCAGGCTGCCAGTCTCC
DNA40370	368	TATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTACTGGTGCCTATG
P_AAC75884	359	TATTTGTGGATAATCCCGTGGGCACTGGGTTTCAGTTATGTGAATGGTACTGGTGCCTATG
DNA40370	428	CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTCTGAAGACCTTCTTCAGTT
P_AAC75884	419	CCAAGGACCTGGCTATGGTGGCTTCAGACATGATGGTTCTCTCTGAAGACCTTCTTCAGTT

BLAST RESULTS A-9

DNA40370	488	GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA *****
P_AAC75884	479	GCCACAAAGAATTCCAGACAGTTCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAA
DNA40370	548	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCA *****
P_AAC75884	539	TGGCAGCTGGCATTGGTCTAGAGCTTTATAAGGCCATTTCAGCGAGGGACCATCAAGTGCA
DNA40370	608	ACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCT *****
P_AAC75884	599	ACTTTGCGGGGGTTGCCTTGGGTGATTTCCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCT
DNA40370	668	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA *****
P_AAC75884	659	GGGGACCTTACCTGTACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTA
DNA40370	728	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC *****
P_AAC75884	719	AGGTTGCAGAGCAAGTACTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGC
DNA40370	788	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA *****
P_AAC75884	779	TGTGGGGGAAAGCAGAAATGATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACA
DNA40370	848	TCTTAACATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC *****
P_AAC75884	839	TCTTAACATAAAAGCACTCCCACGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCC
DNA40370	908	ACCTAGTTTGTCTTTGTCTAGCGCCACGTGAGACACCTACAACGAGATGCCTTAAGCCAGC *****
P_AAC75884	899	ACCTAGTTTGTCTCTGTCTAGCGCCACGTGAGACACCTACAACGAGACGCCTTAAGCCAGC
DNA40370	968	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG *****
P_AAC75884	959	TCATGAATGGCCCCATCAGAAAGAAGCTCAAAATTATTCCTGAGGATCAATCCTGGGGAG
DNA40370	1028	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA *****
P_AAC75884	1019	GCCAGGCTACCAACGTCTTTGTGAACATGGAGGAGGACTTCATGAAGCCAGTCATTAGCA
DNA40370	1088	TTGTGGACGAGTTGCTGGAGGCAGGGATCAACGTGACGGTGTATAATGGACAGCTGGATC *****
P_AAC75884	1079	TTGTGGATACGTTGCTGGAGGCAGGGGTCAATGTGACTGTGTATAATGGGCAGCTGGATC
DNA40370	1148	TCATCGTAGATACCATGGGTTCAGGAGGCCTGGGTGCGGAAACTGAAGTGCCAGAACTGC *****
P_AAC75884	1139	TCATTGTGGACACCATAGGTCAGGAGGCCTGGGTGCGGAAACTGAAGTGCCAGAACTGT
DNA40370	1208	CTAAATTCAGTCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAAACAT *****
P_AAC75884	1199	CCAGATTCAATCAGCTGAAGTGGAAGGCCCTGTACAGTGACCCCTAAATCTTTGGAAACAT
DNA40370	1268	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA *****
P_AAC75884	1259	CTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTCTACTGGATTCTGAAAGCTGGTCATA
DNA40370	1328	TGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG *****
P_AAC75884	1319	TGGTTTCCTTCTGACCAAGGGGACATGGCTCTGAAGATGATGAGACTGGTGACTCAGCAAG
DNA40370	1388	AATAGGATGGATGGGGCTGGAGATGAGCTGCTTTGGCCCTTGGGGGACAGAGCTGAGCTGA *****
P_AAC75884	1379	AATAGGATGGATGGGGCTGGAGATGAGCTGCTTTGGCCCTTGGGGGACAGAGCTGAGCTGA

BLAST RESULTS A-20

DNA40370	1448	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG

P_AAC75884	1439	GGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCTAACTGGGGCTGTGATCAAG
DNA40370	1508	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT

P_AAC75884	1499	AAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCTGGAGGCAATTTGGAAAT
DNA40370	1568	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGT'TTTGATCAAAA

P_AAC75884	1559	TATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGATTGT'TTTGATCAAAA
DNA40370	1628	TAAAGGATGATAATAGATATTA

P_AAC75884	1619	TAAAGGATGATAATAGATATTA

BLAST RESULTS A-21



(B)

Tue Jul 25:23 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpenter/templ/pl.DNA40370 (452 aa)

Sequences producing High-scoring Segment Pairs:

		Score	Match	Pct	E-val
1	E_AAB80255 Human PFO302 protein - Homo sapiens.	2382	452	100	0.0
2	E_AAB20341 Human PFO302 - Homo sapiens.	2382	452	100	0.0
3	F_AAY88378 PFO302, vitellogenic carboxypeptidase hom	2382	452	100	0.0
4	F_AAY13387 protein PFO302 - Homo sapiens.	2382	452	100	0.0
5	F_AAY95768 Human PFO302 (vitellogenic carboxypeptida	2382	452	100	0.0
6	AAG16642.1 serine carboxypeptidase 1 precursor prote	2382	452	100	0.0
7	NP_067639.1 serine carboxypeptidase 1 precursor prote	2382	452	100	0.0
8	P_AAB41675 Human ORFX ORF1439 polypeptide sequence S	2306	439	97	0.0
9	AAG39285.1 MSTP034 - Homo sapiens	2116	402	100	0.0

>1 P_AAB80255 Human PFO302 protein - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370      1 MELALFFSPVFFWLLLLLELLLSLNAGAVIDWPTTEEGKEVWDYVTVFKDAYMFWWLYYATN
*****
P_AAB80255    1 MELALFFSPVFFWLLLLLELLLSLNAGAVIDWPTTEEGKEVWDYVTVFKDAYMFWWLYYATN

DNA40370     61 SCKNFSELEPLVMWLQGGPSSSTGGFGNFEEIGPLDSCLKPRKTTWLQAASLLFVDNPNVGT
*****
P_AAB80255    61 SCKNFSELEPLVMWLQGGPSSSTGGFGNFEEIGPLDSCLKPRKTTWLQAASLLFVDNPNVGT

DNA40370    121 GFDYVIGSGAYAKDLAMVASDMIVLLKTFESCHKEFQTVPFYIFSESYGGRMAAGIGLEL
*****
P_AAB80255   121 GFDYVIGSGAYAKDLAMVASDMIVLLKTFESCHKEFQTVPFYIFSESYGGRMAAGIGLEL

DNA40370    161 YKAIQFGTIEKNEFAGVALSDSWISPVISVLSWGPILYSMSLLEDKGLAEVSEFVAEQVLNA
*****
P_AAB80255   161 YKAIQFGTIEKNEFAGVALSDSWISPVISVLSWGPILYSMSLLEDKGLAEVSEFVAEQVLNA

DNA40370    241 VNEGIYREATPELWGAEMITEQNTDGVNFYNIITKSTPTSTMESSLEFQSHLVCLCQRH
*****
P_AAB80255   241 VNEGIYREATPELWGAEMITEQNTDGVNFYNIITKSTPTSTMESSLEFQSHLVCLCQRH

DNA40370    301 VERHLQFDALSQIMNSPIEFELKIIPEIQSWGGQATNVFVNMEEDENKPVISIVDELLEAG
*****
P_AAB80255   301 VERHLQFDALSQIMNSPIEFELKIIPEIQSWGGQATNVFVNMEEDENKPVISIVDELLEAG

DNA40370    361 INVTVTYNGQLDINVDTEGQEAWVRKLEWPELPKFSQLKWKALYSDPKSLETSAFVKS YKN
*****
P_AAB80255   361 INVTVTYNGQLDINVDTEGQEAWVRKLEWPELPKFSQLKWEALYSDPKSLETSAFVKS YKN

DNA40370    421 LAFYWLKAGRIVRSDQGI MALKMMRLVTQQE
*****
P_AAB80255   421 LAFYWLKAGRIVRSDQGI MALKMMRLVTQQE
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>2 P_AAB20341 Human PFO302 - Homo sapiens. (452 aa) [1 seg]

Score = 2382 (922 bits), Expect = 0.0

Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

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DNA40370      1 MELALFFSPVFFWLLLLLELLLSLNAGAVIDWPTTEEGKEVWDYVTVFKDAYMFWWLYYATN
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BLAST RESULTS B-1

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*****
P_AAB0341 1 MELALFRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKEAYMFWWLYYATN
DNA40370 61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAB0341 61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
*****
P_AAB0341 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKAIQGETIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAB0341 181 YKAIQGETIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGLFEATELWGAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
*****
P_AAB0341 241 VNKGLFEATELWGAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
DNA40370 301 VFHLQFDALSQLMNGPIEFKKLKIIPEIQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAB0341 301 VFHLQFDALSQLMNGPIEFKLEIPEIQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTVNGQLDGLVDITMGQEAWVERLEWPELPEFSQLEWALYSDPESLETSAFVKSYKN
*****
P_AAB0341 361 INVTVNGQLDGLVDITMGQEAWVERLEWPELPEFSQLEWALYSDPESLETSAFVKSYKN
DNA40370 421 LAFTWLIKAGHIVPSDQGMALKMNRIVTQQE
*****
P_AAB0341 421 LAFTWLIKAGHIVPSDQGMALKMNRIVTQQE

```

>3 P_AAY88378 PF0307, v tellogenic carboxypeptidase homologue amino acid
sequence - Homo sapiens. (451 aa) [1 seq]
Score = 2382 (922 bit), Expect = 0.0
Identities = 422/452 (93%), Positives = 452/452 (100%), at 1,1-452,452

```

DNA40370 1 MELALFRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKEAYMFWWLYYATN
*****
P_AAY88378 1 MELALFRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKEAYMFWWLYYATN
DNA40370 61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
*****
P_AAY88378 61 SCNFSESELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
*****
P_AAY88378 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKAIQGETIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY88378 181 YKAIQGETIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGLFEATELWGAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
*****
P_AAY88378 241 VNKGLFEATELWGAEMIIEQNTDGVNFYNILTKSTPTSTNESSLEFTQSHLVCLCQRH
DNA40370 301 VFHLQFDALSQLMNGPIEFKKLKIIPEIQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY88378 301 VFHLQFDALSQLMNGPIEFKLEIPEIQSWGGQATNVFVNMEEDFMKPVISIVDELLEAG

```

BLAST RESULTS B-2

BLAST RESULTS B-3

```
*****
P_AAY88378 301 VRHLQFLALSQLMNGPIRKKLKIIPEIQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVEKLEWPELPEFSQLEKWKALYSDPKSLETSAFVKSYKH
*****
P_AAY88378 361 INVTVYNGQLDLIVDTMGQEAWVEKLEWPELPEFSQLEKWKALYSDPKSLETSAFVKSYKH
DNA40370 411 LAFYWILEAGHMVPSDQGMALKNMRLVTQQE
*****
P_AAY88378 411 LAFYWILEAGHMVPSDQGMALKNMRLVTQQE
```

>4 P_AAY13387 protein PF0302 - Homo sapiens. (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370 1 MELALFEESPVFWLWLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFHDAYMFWWLYYATH
*****
P_AAY13387 1 MELALFEESPVFWLWLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFHDAYMFWWLYYATH
DNA40370 61 SKKNESELPLVMWLQGGPGSSSTGFGNFEEIGPLDSCLKPKKTTWLQAASLLFVDNPVGT
*****
P_AAY13387 61 SKKNESELPLVMWLQGGPGSSSTGFGNFEEIGPLDSCLKPKKTTWLQAASLLFVDNPVGT
DNA40370 121 GESYVNGSGAYAKDLAMVASDMNVLLFTFEESCHKEFQTVPFYIFSLFYGGKMAAGIGLEL
*****
P_AAY13387 121 GESYVNGSGAYAKDLAMVASDMNVLLFTFEESCHKEFQTVPFYIFSLFYGGKMAAGIGLEL
DNA40370 181 YHAIQEGTIKCNFAGVALQDSWLSFVLSVLSWGPYLYSMILLEDEKGLAEVSKVAEQVLNA
*****
P_AAY13387 181 YHAIQEGTIKCNFAGVALQDSWLSFVLSVLSWGPYLYSMILLEDEKGLAEVSKVAEQVLNA
DNA40370 241 VNEGLYEATEIWGFAEMIIEQNTDGVNFYNIILTKSTPTSTNESSLEFTQSHLVCLCQRI
*****
P_AAY13387 241 VNEGLYEATEIWGFAEMIIEQNTDGVNFYNIILTKSTPTSTNESSLEFTQSHLVCLCQRI
DNA40370 301 VRHLQFDALSQIMNCPIRKKLKIIPEIQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
*****
P_AAY13387 301 VRHLQFDALSQIMNCPIRKKLKIIPEIQSWGQATNVFVNMEEDFMKPVISIVDELLEAG
DNA40370 361 INVTVYNGQLDIIVDTMGQEAWVEKLEWPELPEFSQLEKWKALYSDPKSLETSAFVKSYKH
*****
P_AAY13387 361 INVTVYNGQLDIIVDTMGQEAWVEKLEWPELPEFSQLEKWKALYSDPKSLETSAFVKSYKH
DNA40370 411 LAFYWILKAGHMVPSDQGMALKNMRLVTQQE
*****
P_AAY13387 411 LAFYWILKAGHMVPSDQGMALKNMRLVTQQE
```

>5 P_AAY05768 Human PKnox1 (vitellogenin carboxypeptidase homologue) - Homo (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370 1 MELALFEESPVFWLWLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFHDAYMFWWLYYATH
*****
P_AAY05768 1 MELALFEESPVFWLWLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVFHDAYMFWWLYYATH
DNA40370 61 SKKNESELPLVMWLQGGPGSSSTGFGNFEEIGPLDSCLKPKKTTWLQAASLLFVDNPVGT
```


BLAST RESULTS B-A

```
*****
P_AAY05768 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDPNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
P_AAY05768 121 GFSYVNGSGAYAKDLAMVASDMMVLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKAIQPGTIRKCNFAGVALGDSWISFVLSVLSWSPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
P_AAY05768 181 YKAIQPGTIRKCNFAGVALGDSWISFVLSVLSWSPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGLYFEATELWGF AEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
P_AAY05768 241 VNKGLYFEATELWGF AEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VEHLQFDALSQLMNGPIRKKELKIIIFELQSWGQATNVFVNMEEDFMKPVISIVDEILLEAG
*****
P_AAY05768 301 VEHLQFDALSQLMNGPIRKKELKIIIFELQSWGQATNVFVNMEEDFMKPVISIVDEILLEAG
DNA40370 361 INVTVYNGQLDLIVDTMQQFAWVRFLLKWPPELKFESQLKWKALYSDPKSLETSAFVKSYKN
*****
P_AAY05768 361 INVTVYNGQLDLIVDTMQQFAWVRFLLKWPPELKFESQLKWKALYSDPKSLETSAFVKSYKN
DNA40370 421 LAFYWLKAGHMVPCDQGMALKMNNRENTQQE
*****
P_AAY05768 421 LAFYWLKAGHMVPCDQGMALKMNNRENTQQE
```

>6 AAG16692.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seg]
Score = 2382 (922 bits), Expect = 0.0
Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```
DNA40370 1 MELALRESEVPFWLLILLPLILLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
*****
AAG16692.1 1 MELALRESEVPFWLLILLPLILLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
DNA40370 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDPNPVGT
*****
AAG16692.1 61 SCKNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDPNPVGT
DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
*****
AAG16692.1 121 GFSYVNGSGAYAKDLAMVASDMMVLKTTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
DNA40370 181 YKAIQPGTIRKCNFAGVALGDSWISFVLSVLSWSPYLYSMSLLEDKGLAEVSKVAEQVLNA
*****
AAG16692.1 181 YKAIQPGTIRKCNFAGVALGDSWISFVLSVLSWSPYLYSMSLLEDKGLAEVSKVAEQVLNA
DNA40370 241 VNKGLYFEATELWGF AEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
*****
AAG16692.1 241 VNKGLYFEATELWGF AEMII EQNTDGVNFYNI LTKSTPTSTMESSLEFTQSHLVCLCQRH
DNA40370 301 VEHLQFDALSQLMNGPIRKKELKIIIFELQSWGQATNVFVNMEEDFMKPVISIVDEILLEAG
*****
AAG16692.1 301 VEHLQFDALSQLMNGPIRKKELKIIIFELQSWGQATNVFVNMEEDFMKPVISIVDEILLEAG
DNA40370 361 INVTVYNGQLDLIVDTMQQFAWVRFLLKWPPELKFESQLKWKALYSDPKSLETSAFVKSYKN
*****
AAG16692.1 361 INVTVYNGQLDLIVDTMQQFAWVRFLLKWPPELKFESQLKWKALYSDPKSLETSAFVKSYKN
```

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*****
AAG16692.1 361 INVTVYNGQLDLIVDTMGQEAWVEKWKWPELPKFSQLKWKALYSDPKSLETSFVKS YKN
      DNA40370 421 LAFYWILKAGHMVPSDQGMALKMMPLVTQGE
      *****
AAG16692.1 411 LAFYWILKAGHMVPSDQGMALKMMELVTQGE

```

>7 NP_067639.1 serine carboxypeptidase 1 precursor protein - Homo sapiens (452 aa) [1 seq]
 Score = 2382 (922 bits), Expect = 0.0
 Identities = 452/452 (100%), Positives = 452/452 (100%), at 1,1-452,452

```

      DNA40370      1 MELALHESPVERWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
      *****
NP_067639.1      1 MELALHESPVERWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

      DNA40370     61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT
      *****
NP_067639.1     61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT

      DNA40370    121 GFSYVDSGAYAKDLAMVASDMMVLLKTFEFSCHKEFQTVPFYIFSESYGKMAAGIGLEL
      *****
NP_067639.1    111 GFSYVDSGAYAKDLAMVASDMMVLLKTFEFSCHKEFQTVPFYIFSESYGKMAAGIGLEL

      DNA40370    181 YKATQFGTIKCNFAGVALGDSWIEPVLGVLCWGPYLYSMSLLEDKGLAEVSKVAEQVLNA
      *****
NP_067639.1    181 YKATQFGTIKCNFAGVALGDSWIEPVLGVLCWGPYLYSMSLLEDKGLAEVSKVAEQVLNA

      DNA40370    241 VNEGLYFEATELWGAEMII EQNTDGVNFEYNILTESTPTSTHESSELEFTQSHLVCLCQRH
      *****
NP_067639.1    241 VNEGLYFEATELWGAEMII EQNTDGVNFEYNILTESTPTSTHESSELEFTQSHLVCLCQRH

      DNA40370    301 VEHLQFQDALSQLMNGEPIEFKLKIIPEIQSWGGQATNVFVNMEEDEMEKEFVISIVDELLEAG
      *****
NP_067639.1    301 VEHLQFQDALSQLMNGEPIEFKLKIIPEIQSWGGQATNVFVNMEEDEMEKEFVISIVDELLEAG

      DNA40370    361 INVTVYNGQLDLIVDTMGQEAWVEKWKWPELPKFSQLKWKALYSDPKSLETSFVKS YKN
      *****
NP_067639.1    361 INVTVYNGQLDLIVDTMGQEAWVEKWKWPELPKFSQLKWKALYSDPKSLETSFVKS YKN

      DNA40370    421 LAFYWILKAGHMVPSDQGMALKMMELVTQGE
      *****
NP_067639.1    411 LAFYWILKAGHMVPSDQGMALKMMELVTQGE

```

>8 P_AAB41675 Human ORFX ORF144 polypeptide sequence SEQ ID NO: 873 - Homo (451 aa) [1 seq]
 Score = 2506 (892 bits), Expect = 0.0
 Identities = 449/452 (99%), Positives = 444/452 (98%), Gaps = 1/452 (0%), at 1,1-452,451

```

      DNA40370      1 MELALHESPVERWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN
      *****
P_AAB41675      1 MELALHESPVERWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATN

      DNA40370     61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT
      *****
P_AAB41675     61 SCKNEFELPLVMWLQGGPGGSSSTGPGNFEEIGPLDSULKPEKTTWLQAASLLFVDNIPVGT

```

DNA40370 121 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL
 P_AAB41675 120 GFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGGKMAAGIGLEL

DNA40370 181 YFAIQPGTIFKCNFAGVALGDSWISPVDSVLSWGPYLYSM S LLEDKGLAEVSKVAEQVLNA
 P_AAB41675 180 YFAIQPGTIFKCNFAGVALGDSWISPVDSVLSWGPYLYSM S LLEDKGLAEVSKVAEQVLNA

DNA40370 241 VNKGlyFEATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQSHLVCLCQRH
 P_AAB41675 240 VNKGlyFEATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQSHLVCLCQRH

DNA40370 301 VERHLQFDALSQLNNGPIRKELKIIFEDQSWGGQATNVFVIM EEDFMKPVISIVDELLLEAG
 P_AAB41675 300 VERHLQFDALSQLNNGPIRKELKIIFEDQSWGGQATNVFVIM EEDFMKPVIDIVDTLLEAG

DNA40370 361 INVTVYNGQLDLIVDTMGQEAWVRKLEWPEL PKFSQ LKWKALYS DPKSLETS AFVKSYKN
 P_AAB41675 360 INVTVYNGQLDLIVDTMGQEAWVRKLEWPEL SEFNQLKWKALYS DPKSLETS AFVKSYKN

DNA40370 411 LAFYWILKAGEMVPSDQGMALKMMRLVTDQE
 P_AAB41675 410 LAFYWILKAGEMVPSDQGMALKMMRLVTDQE

>9 AAG39285.1 M8TP034 - Homo sapiens (407 aa) [1 seg]
 Score = 2116 (319 bits), Expect = 0.0
 Identities = 402/402 (100%), Positives = 402/402 (100%), at 51,1-452,402

DNA40370 51 MFWWLYYATNSCHNFSELI LVMWLQGGPGGISTGFGHPEEIGPLISDLKPKRTTWLQAAS
 AAG39285.1 1 MFWWLYYATNSCHNFSELI LVMWLQGGPGGISTGFGHPEEIGPLISDLKPKRTTWLQAAS

DNA40370 111 LLEFVDHPVGTGFTFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGG
 AAG39285.1 61 LLEFVDHPVGTGFTFSYVNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSES YGG

DNA40370 181 KMAAGSGLLELYKALQPGTIFKCNFAGVALGDSWISPVDSVLSWGPYLYSM S LLEDKGLAEV
 AAG39285.1 111 KMAAGSGLLELYKALQPGTIFKCNFAGVALGDSWISPVDSVLSWGPYLYSM S LLEDKGLAEV

DNA40370 231 SKVAEQVLNAVNHGLYREATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQ
 AAG39285.1 181 SKVAEQVLNAVNHGLYREATELWGFaEMIIEQNTDGVNfYNIILTKSTPTSTMESSLEFTQ

DNA40370 291 SHLVCLCQELVERHLQFDALSQLNNGPIRKELKIIFEDQSWGGQATNVFVIM EEDFMKPVISIVDELLLEAG
 AAG39285.1 241 SHLVCLCQELVERHLQFDALSQLNNGPIRKELKIIFEDQSWGGQATNVFVIM EEDFMKPVISIVDELLLEAG

DNA40370 351 SIVDELLLEAGSINVTVYNGQLDLIVDTMGQEAWVRKLEWPEL PKFSQ LKWKALYS DPKSLETS AFVKSYKN
 AAG39285.1 361 SIVDELLLEAGSINVTVYNGQLDLIVDTMGQEAWVRKLEWPEL SEFNQLKWKALYS DPKSLETS AFVKSYKN

DNA40370 411 LAFYWILKAGEMVPSDQGMALKMMRLVTDQE
 AAG39285.1 411 LAFYWILKAGEMVPSDQGMALKMMRLVTDQE

BLAST RESULTS B-6